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gcgtctccac ccctcagcgg gcggcggtga gtgcgccagg ccagcgccgg cgtgggaccg
 61 agcggcgtg aaggcgcgag ctgaacgctg gcacggtttc ctagatctaa aagaaaggcc
121 gagttagagt accettcaa AATGGCTGCT ATTAAGGAAG AGAGAGAGGT GGAAGATTAC
 121 AAGAGAAAAA GGAAGACGAT CAGCACAGGC CATGAGCCTA AGGAGCCACA GCAGTTGAGA
241 AAGCTGTTCA TTGGAGGTCT GAGCTTCGAG ACGACGGATG ATAGCTTGAG AGAGCACTTT
 301 GAAAAATGGG GCACACTCAC GGACTGTGTG GTGATGAGAG ACCCACAAAC AAAACGTTCC
 361 AGAGGCTTTG GCTTTGTTAC TTACTCTTGC GTGGAAGAGG TGGATGCGGC CATGAGCGCT
 421 CGACCACATA AGGTGGATGG ACGTGTGGTT GAACCAAAGA GAGCAGTTTC AAGGGAGGAT
 481 TCTGTAAAGC CTGGGGCGCA TCTCACAGTA AAGAAAATAT TTGTTGGTGG CATTAAAGAA
 541 GATACAGANG AATATAATTT AAGGGGGTAC TITGAAACAT ATGGCAAGAT GGAAACGATA
601 GAAGTCATGG AAGACAGACA AAGTGGAAAG AAAAGAGGCT TCGCTTTTGT AACTTTTGAT
 661 GATCACGATA CAGTTGATAA AATTGTTGTT CAGAAATACC ATACTATAAA TGGTCATAAC
 721 TGCGAAGATA AAAAAGCACT CTCAAAACAA GAGATGCAGA CTGCCAGCTC TCAGAGAGGT
 781 CGTGGGGGTG GTTCAGGCAA CTTCATGGGT CGTGGAAATT TTGGAGGTGG TGGAGGAAAC
 841 TTTGGCCGAG GAGGAAACTT TGGTGGAAGA GGAGGCTATG GGGGTGGTGG TGGCGGTGGT
 901 GGGAGCAGAG GAAGCTTTGG GGGTGGTGAT GGATACAACG GATTTGGTGA TGGTGGCAAC
 961 TATGGAGGTG GTCCTGGCTA TGGCAGCAGA GGGGGTTATG GTGGTGGTGG AGGACCAGGA
1021 TATGGAAACC CAGGTGGTGG ATATGGAGGT GGAGGAGGAG GATATGGTGG CTACAATGAA
1081 GGAGGCAATT TTGGAGGTGG TAATTATGGA GGCAGTGGAA ACTACAATGA CTTTGGTAAC
1141 TACAGTGGAC AGCAGCAGTC CAATTACGGT CCCATGAAAG GTGGTGGCAG TTTTGGTGGT
1201 AGAAGTTCAG GCAGTCCCTA TGGTGGTGGT TATGGATCTG GAAGTGGAAG TGGGGGCTAT
1261 GGTGGTAGAA GATTCTaaaa atgctaccag aaaaagggct acagttctta gcaggagaga
1321 gagcgaggag ttgtcaggaa agctgcaggt tactttgaga cagtcgtccc aaatgcatta
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1621 ttgtggtagt ggtaccagga ataaacaaat taaggaattt ttggcttttc aaaaaaaaa
1681 aaaaaaaaa
```

## Fig. 1a

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- MAAIKEEREVEDYKRKRKTISTGHEPKEPEQLRKLFIGGLSFETTDDSLR
CHKA1
                        -----SKSESPKEPEOLRKLFIGGLSFETTDESLR
HUMA1
     - EOFEKWGTLTDCVVMRDPQTKRSRGFGFVTYSCVEEVDAAMSARPHKVDG -100
CHKA1
      HUMA1
     - RVVEPKRAVSREDSVKPGAHLTVKKIFVGGIKEDTEEYNLRGYFETYGKI -150
CHKA1
       RVVEPKRAVSREDSQRPGAHLTVKKIFVGGIKEDTEEHHLRDYFEQYGKI -131
HUMA1
     - ETIEVMEDRQSGKKRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEDKKAL -200
CHKA1
     HUMA1
     - SKQEMQTASS-QRGRGGGSGNFMGRGNFGGGGG-----NFGRGGNFGG -242
CHKA1
     - SKQEMASASSSQRGRSGS-----GNFGGGRGGGFGGNDNFGRGGNFSG -224
HUMA1
       RGGYGGGGGGGSRGSFGGDGYNGFGDGGNYGGGPGYGSRGGYGGGGGP -292
CHKA1
      HUMA1
     - GYGNPGGGYGGGGGGYGGYNEGGNFGGGNYGGSGNYNDFGNYSGQQQSNY -342
CHKA1
           HUMA1
     - GPMKGGGSFGGRSSGSPYGGG------YGSGSGSGSGYG-GRRF
CHKA1
       THE REPORT OF
       GPMKGG-NFGGRSSG-PYGGGGQYFAKPRNQGGYGGSSSSSSYGSGRRF
HUMA1
```

Fig.1b

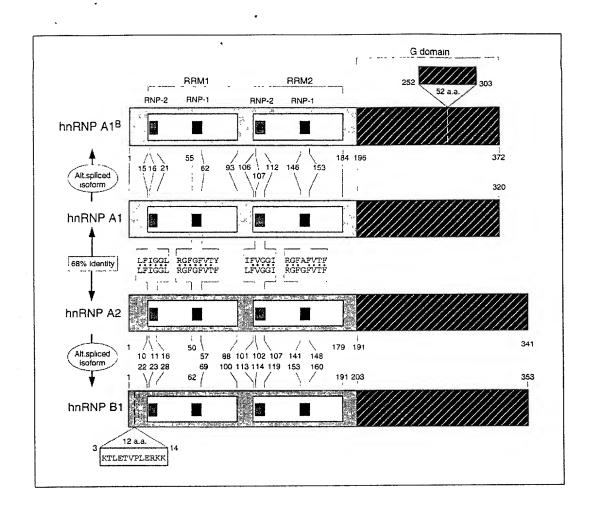


Fig. 2

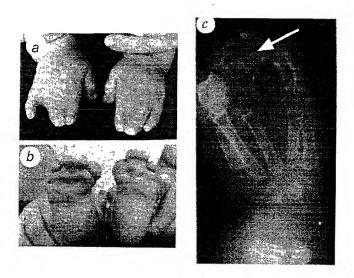


Fig. 3

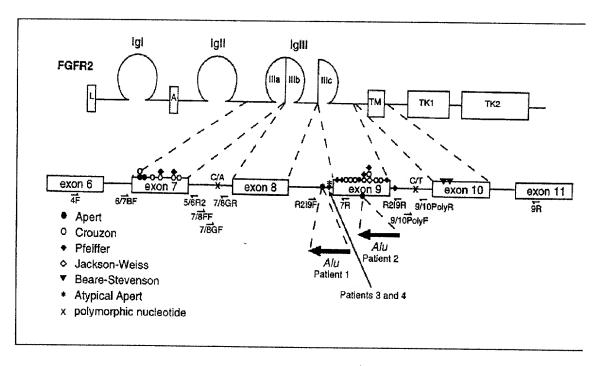
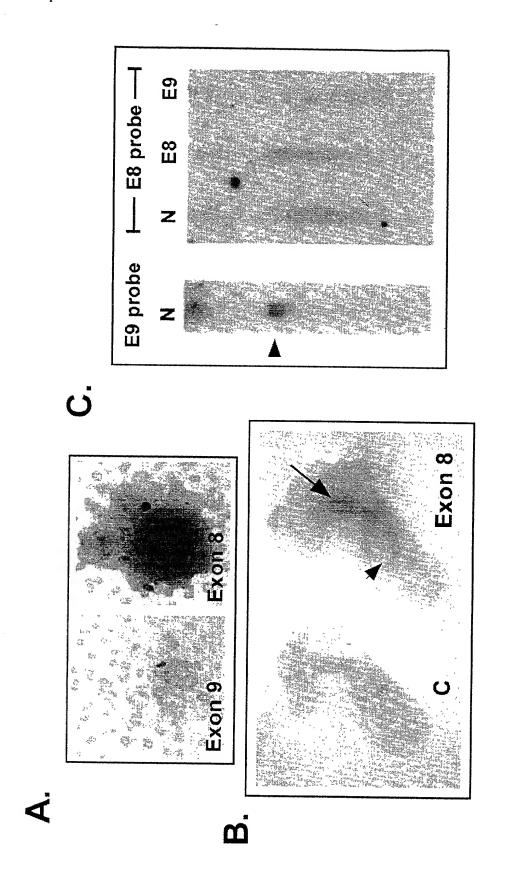


Fig. 4



F19.5